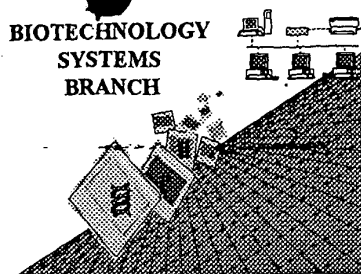BIOTECHNOLOGY
SYSTEMS
BRANCH

# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/659,983_

Source: _OIPE_

Date Processed by STIC: _9/25/2000_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

# Raw Sequence Listing Error Summary

ERROR DETECTED    SUGGESTED CORRECTION    SERIAL NUMBER: _09/659,983_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos    The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length    The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _✓_ Misaligned Amino Acid Numbering    The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _✓_ Non-ASCII    This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _✓_ Variable Length    Sequence(s) _3_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)    Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
**(2) INFORMATION FOR SEQ ID NO:X:**
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**
**This sequence is intentionally skipped**

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)    Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
**<210> sequence id number**
**<400> sequence id number**
**000**

10 _____ Use of n's or Xaa's (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)    Sequence(s) _____ are missing this mandatory field or its response.

_3,4 5,6,7—13_

12 _✓_ Use of <220>Feature (NEW RULES)    Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
**Please explain source of genetic material in <220> to <223> section.**
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)    (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"    **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

*see item 5 on Error Summary Sheet*

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION:  US/09/659,983

DATE: 09/25/2000  
TIME: 12:45:58

**Does Not Comply  
Corrected Diskette Needed**

Input Set : A:\ES.txt  
Output Set: N:\CRF3\09252000\I659983.raw

```
 4 <110> APPLICANT: Meloen, Robert Hans
 6        Oonk, Hendrica Berendina
 9 <120> TITLE OF INVENTION: An Improved Peptide, Immunogenic Composition and Vaccine or Medical
10        Preparation, a Method to Immunise Animals Against the Hormone LHRH, and
11        Analogs of the LHRH Tandem Repeat Peptide and their Use as Vaccine
14 <130> FILE REFERENCE: 2183-4518US
17 <140> CURRENT APPLICATION NUMBER: US/09/659,983
19 <141> CURRENT FILING DATE: 2000-09-12
22 <150> PRIOR APPLICATION NUMBER: US 09/274,048
24 <151> PRIOR FILING DATE: 1999-03-22
27 <150> PRIOR APPLICATION NUMBER: US 08/981,557
29 <151> PRIOR FILING DATE: 1995-06-07
32 <150> PRIOR APPLICATION NUMBER: PCT/NL96/00223
34 <151> PRIOR FILING DATE: 1996-06-06
37 <150> PRIOR APPLICATION NUMBER: US 08/447,298
39 <151> PRIOR FILING DATE: 1995-06-07
42 <150> PRIOR APPLICATION NUMBER: US 08/476,013
44 <151> PRIOR FILING DATE: 1995-06-07
47 <160> NUMBER OF SEQ ID NOS: 13
50 <170> SOFTWARE: Corel WordPerfect 8.0
```

*Please consult new Sequence Rules.*

ERRORED SEQUENCES

```
      53 <210> SEQ ID NO: 1
      55 <211> LENGTH: 10
E--> 57 <212> TYPE: peptide
      59 <213> ORGANISM: Sus scrofa
      61 <220> FEATURE:
W--> 63 <221> NAME/KEY: Xaa
      65 <222> LOCATION: 1
      67 <223> OTHER INFORMATION: pyroglutamic acid
W--> 69 <221> NAME/KEY: Xaa
      71 <222> LOCATION: 10
      73 <223> OTHER INFORMATION: Gly-NH2
      75 <400> SEQUENCE: 1
      77        Xaa His Trp Ser Tyr Gly Leu Arg Pro Xaa
      78        1               5                   10
      81 <210> SEQ ID NO: 2
      83 <211> LENGTH: 10
E--> 85 <212> TYPE: peptide
      87 <213> ORGANISM: Homo sapiens
      89 <220> FEATURE:
W--> 91 <221> NAME/KEY: Xaa
      93 <222> LOCATION: 1
      95 <223> OTHER INFORMATION: pyroglutamic acid
W--> 97 <221> NAME/KEY: Xaa
```

*invalid response - use PRT*

*e.s. Xaa is pyroglutamic acid — move down use, preferably, Appendix 2, Table 6, of WIPO Standard ST.25, for identifier*

```
                    RAW SEQUENCE LISTING            DATE: 09/25/2000
                    PATENT APPLICATION:  US/09/659,983    TIME: 12:45:58

                    Input Set : A:\ES.txt
                    Output Set: N:\CRF3\09252000\I659983.raw

      99 <222> LOCATION: 10
     101 <223> OTHER INFORMATION: Gly-NH2
     103 <400> SEQUENCE: 2
     105     Xaa His Trp Ser His Gly Trp Tyr Pro Xaa
     106     1           5                   10
     110 <210> SEQ ID NO: 3
     112 <211> LENGTH: variable
E--> 114 <212> TYPE: peptide
     116 <213> ORGANISM: artificial
     118 <220> FEATURE:
W--> 120 <221> NAME/KEY: Xaa
     122 <222> LOCATION: 1
     124 <223> OTHER INFORMATION: pyroglutamic acid or Gln with attached tail of one or more additional
     125     amino acids
W--> 127 <221> NAME/KEY: Xaa
     129 <222> LOCATION: 3
     131 <223> OTHER INFORMATION: Trp or N(indole)formyl-tryptophan
W--> 133 <221> NAME/KEY: Xaa
     135 <222> LOCATION: 13
     137 <223> OTHER INFORMATION: Trp or N(indole)formyl-tryptophan
W--> 139 <221> NAME/KEY: Xaa
     141 <222> LOCATION: 20
     143 <223> OTHER INFORMATION: Gly-NH2 or Gly with attached tail of one or more amino acids
W--> 145 <221> NAME/KEY: X
     147 <222> LOCATION: 11
     149 <223> OTHER INFORMATION: direct bond or a spacer group between Gly at position 10 and Gln at
     150     position 11
W--> 152 <221> NAME/KEY: n
     154 <222> LOCATION: 20
     156 <223> OTHER INFORMATION: integer greater than or equal to 1 indicating number of repeats of
     157     sequence at positions 10 to 19
     159 <400> SEQUENCE: 3
     161     Xaa His Xaa Ser Tyr Gly Leu Arg Pro Gly X Gln His Xaa Ser Tyr Gly
     162     1               5                   10          15
     163     Leu Arg Pro Xaa
     164                 20
     167 <210> SEQ ID NO: 4
     169 <211> LENGTH: 21
E--> 171 <212> TYPE: peptide
     173 <213> ORGANISM: artificial
     175 <220> FEATURE:
W--> 177 <221> NAME/KEY: Xaa
     179 <222> LOCATION: 1
     181 <223> OTHER INFORMATION: pyroglutamic acid
W--> 183 <221> NAME/KEY: Xaa
     185 <222> LOCATION: 6
     187 <223> OTHER INFORMATION: D-Lys
W--> 189 <221> NAME/KEY: Xaa
     191 <222> LOCATION: 11
```

*Handwritten annotations:* This is not an acceptable response — variable length is not permitted (see item 6 on Error Summary Sheet). (give an integer) see item 12 on Error Summary Sheet. do not show this in the sequence. It can be explained in <220>, <223> section. delete — only show amino acids. delete delete. delete. see item 6 on Error Summary Sheet. see item 12.

RAW SEQUENCE LISTING          DATE: 09/25/2000
PATENT APPLICATION: US/09/659,983      TIME: 12:45:58

Input Set : A:\ES.txt
Output Set: N:\CRF3\00252000\ ～

```
          193 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer    OK
W--> 195 <221> NAME/KEY: Xaa
          197 <222> LOCATION: 16
          199 <223> OTHER INFORMATION: D-Lys
W--> 201 <221> NAME/KEY: Xaa
          203 <222> LOCATION: 21
          205 <223> OTHER INFORMATION: Cys-NH2                ) delete - no Xaa's after location 21
W--> 207 <221> NAME/KEY: Xaa
          210 <400> SEQUENCE: 4
          212       Xaa His Trp Ser Tyr Xaa Leu Arg Pro Gly Xaa His Trp Ser Tyr Xaa
          213       1           5                  10   OK        15
          214       Leu Arg Pro Gly Xaa
          215                   20
          218 <210> SEQ ID NO: 5
          220 <211> LENGTH: 21
E--> 222 <212> TYPE: peptide             item 12
          224 <213> ORGANISM: artificial
          226 <220> FEATURE:
W--> 228 <221> NAME/KEY: Xaa
          230 <222> LOCATION: 1
          232 <223> OTHER INFORMATION: pyroglutamic acid
W--> 234 <221> NAME/KEY: Xaa
          236 <222> LOCATION: 4
          238 <223> OTHER INFORMATION: amino acid substitution
W--> 240 <221> NAME/KEY: Xaa
          242 <222> LOCATION: 6
          244 <223> OTHER INFORMATION: D-Lys
W--> 246 <221> NAME/KEY: Xaa
          248 <222> LOCATION: 11           OK
          250 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 252 <221> NAME/KEY: Xaa
          254 <222> LOCATION: 14
          256 <223> OTHER INFORMATION: amino acid substitution
W--> 258 <221> NAME/KEY: Xaa
          260 <222> LOCATION: 16
          262 <223> OTHER INFORMATION: D-Lys
W--> 264 <221> NAME/KEY: Xaa
          266 <222> LOCATION: 21
          268 <223> OTHER INFORMATION: Cys-NH2
          270 <400> SEQUENCE: 5
          272       Xaa His Trp Xaa Tyr Xaa Leu Arg Pro Gly Xaa His Trp Xaa Tyr Xaa
          273       1           5                  10          15
          274       Leu Arg Pro Gly Xaa
          275                   20
          278 <210> SEQ ID NO: 6
          280 <211> LENGTH: 21
E--> 282 <212> TYPE: peptide             item 12
          284 <213> ORGANISM: artificial
          286 <220> FEATURE:
```

```
            RAW SEQUENCE LISTING              DATE: 09/25/2000
            PATENT APPLICATION:  US/09/659,983    TIME: 12:45:58

            Input Set : A:\ES.txt
            Output Set: N:\CRF3\09252000\I659983.raw

W--> 288 <221> NAME/KEY: Xaa
     290 <222> LOCATION: 1
     292 <223> OTHER INFORMATION: pyroglutamic acid
W--> 294 <221> NAME/KEY: Xaa
     296 <222> LOCATION: 6
     298 <223> OTHER INFORMATION: D-Lys
W--> 300 <221> NAME/KEY: Xaa
     302 <222> LOCATION: 8
     304 <223> OTHER INFORMATION: amino acid substitution
W--> 306 <221> NAME/KEY: Xaa                    OK
     308 <222> LOCATION: 11
     310 <223> OTHER INFORMATION: Gly (or Gly) preceded by a spacer
W--> 312 <221> NAME/KEY: Xaa
     314 <222> LOCATION: 16
     316 <223> OTHER INFORMATION: D-Lys
W--> 318 <221> NAME/KEY: Xaa
     320 <222> LOCATION: 18
     322 <223> OTHER INFORMATION: amino acid substitution
W--> 324 <221> NAME/KEY: Xaa
     326 <222> LOCATION: 21
     328 <223> OTHER INFORMATION: Cys-NH2
     331 <400> SEQUENCE: 6
     333      Xaa His Trp Ser Tyr Xaa Leu Xaa Pro Gly Xaa His Trp Ser Tyr Xaa
     334      1               5               10              15
     335      Leu Xaa Pro Gly Xaa
     336                   20
     339 <210> SEQ ID NO: 7
     341 <211> LENGTH: 21
E--> 343 <212> TYPE: peptide
     345 <213> ORGANISM: artificial
     347 <220> FEATURE:
W--> 349 <221> NAME/KEY: Xaa
     351 <222> LOCATION: 1
     353 <223> OTHER INFORMATION: pyroglutamic acid
W--> 355 <221> NAME/KEY: Xaa
     357 <222> LOCATION: 6
     359 <223> OTHER INFORMATION: D-Lys
W--> 361 <221> NAME/KEY: Xaa
     363 <222> LOCATION: 10
     365 <223> OTHER INFORMATION: amino acid substitution
W--> 367 <221> NAME/KEY: Xaa
     369 <222> LOCATION: 11
     371 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 373 <221> NAME/KEY: Xaa
     375 <222> LOCATION: 20
     377 <223> OTHER INFORMATION: amino acid substitution
W--> 379 <221> NAME/KEY: Xaa
     381 <222> LOCATION: 21
     383 <223> OTHER INFORMATION: Cys-NH2
```

*what about Xaa at location 16?*
*(next page)*

RAW SEQUENCE LISTING      DATE: 09/25/2000
PATENT APPLICATION:   US/09/659,983     TIME: 12:45:58

Input Set : A:\ES.txt
Output Set: N:\CRF3\09252000\I659983.raw

```
385 <400> SEQUENCE: 7
387       Xaa His Trp Ser Tyr Xaa Leu Arg Pro Xaa Xaa His Trp Ser Tyr Xaa
388       1             5                      10                  15
389       Leu Arg Pro Xaa Xaa
390                   20
393 <210> SEQ ID NO: 8
395 <211> LENGTH: 42
E--> 397 <212> TYPE: peptide
399 <213> ORGANISM: artificial
401 <220> FEATURE:
W--> 403 <221> NAME/KEY: Xaa
405 <222> LOCATION: 1
407 <223> OTHER INFORMATION: Glu-NH2
W--> 409 <221> NAME/KEY: Xaa
411 <222> LOCATION: 6
413 <223> OTHER INFORMATION: D-Lys
W--> 415 <221> NAME/KEY: Xaa
417 <222> LOCATION: 11
419 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 421 <221> NAME/KEY: Xaa
423 <222> LOCATION: 16
425 <223> OTHER INFORMATION: D-Lys
W--> 427 <221> NAME/KEY: Xaa
429 <222> LOCATION: 22
431 <223> OTHER INFORMATION: Glu-NH2
W--> 433 <221> NAME/KEY: Xaa
435 <222> LOCATION: 27
437 <223> OTHER INFORMATION: D-Lys
W--> 439 <221> NAME/KEY: Xaa
441 <222> LOCATION: 32
443 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 445 <221> NAME/KEY: Xaa
447 <222> LOCATION: 37
449 <223> OTHER INFORMATION: D-Lys
   451 <221> NAME/KEY: misc-structure
453 <222> LOCATION: 21
455 <223> OTHER INFORMATION: dimer formed between Cys at 21 to Cys at 42
457 <400> SEQUENCE: 8
459   Xaa His Trp Ser Tyr Xaa Leu Arg Pro Gly Xaa His Trp Ser Tyr Xaa
460     1             5                    10                   15
461       Leu Arg Pro Gly Cys Xaa His Trp Ser Tyr Xaa Leu Arg Pro Gly Xaa
462                   20                    25                  30
463       His Trp Ser Tyr Xaa Leu Arg Pro Gly Cys
464                   35                  40
468 <210> SEQ ID NO: 9
470 <211> LENGTH: 21
E--> 472 <212> TYPE: peptide
474 <213> ORGANISM: artificial
476 <220> FEATURE:
```

*[handwritten annotations in right margin:]* use underscore, not hyphen   misc_structure

*[handwritten annotation:]* misaligned amino acid nos. - see item 4 on Error Summary sheet

```
                    RAW SEQUENCE LISTING              DATE: 09/25/2000
                    PATENT APPLICATION:  US/09/659,983    TIME: 12:45:58

                    Input Set : A:\ES.txt
                    Output Set: N:\CRF3\09252000\I659983.raw

W--> 478 <221> NAME/KEY: Xaa
     480 <222> LOCATION: 1
     482 <223> OTHER INFORMATION: pyroglutamic acid
W--> 484 <221> NAME/KEY: Xaa
     486 <222> LOCATION: 6
     488 <223> OTHER INFORMATION: D-Lys
W--> 490 <221> NAME/KEY: Xaa
     492 <222> LOCATION: 11
     494 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 496 <221> NAME/KEY: Xaa
     498 <222> LOCATION: 16
     500 <223> OTHER INFORMATION: D-Lys
W--> 502 <221> NAME/KEY: Xaa
     504 <222> LOCATION: 21
     506 <223> OTHER INFORMATION: Cys-NH2
     508 <400> SEQUENCE: 9
     510      Xaa His Trp Ser Tyr Xaa Leu Arg Pro Gly Xaa His Trp Ser Tyr Xaa
     511      1               5                   10                  15
     512      Leu Arg Pro Gly Xaa
     513                   20
     515 <210> SEQ ID NO: 10
     517 <211> LENGTH: 21
E--> 519 <212> TYPE: peptide
     521 <213> ORGANISM: artificial
     523 <220> FEATURE:
W--> 525 <221> NAME/KEY: Xaa
     527 <222> LOCATION: 1
     529 <223> OTHER INFORMATION: amino acid substitution with acetyl group
W--> 531 <221> NAME/KEY: Xaa
     533 <222> LOCATION: 6
     535 <223> OTHER INFORMATION: D-Lys
W--> 537 <221> NAME/KEY: Xaa
     539 <222> LOCATION: 11
     541 <223> OTHER INFORMATION: amino acid substitution
W--> 543 <221> NAME/KEY: Xaa
     545 <222> LOCATION: 16
     547 <223> OTHER INFORMATION: D-Lys
W--> 549 <221> NAME/KEY: Xaa
     551 <222> LOCATION: 21
     553 <223> OTHER INFORMATION: Cys-NH2
     555 <400> SEQUENCE: 10
     556      Xaa His Trp Ser Tyr Xaa Leu Arg Pro Gly Xaa His Trp Ser Tyr Xaa
     557      1               5                   10                  15
     558      Leu Arg Pro Gly Xaa
     559                   20
     562 <210> SEQ ID NO: 11
     564 <211> LENGTH: 21
E--> 566 <212> TYPE: peptide
     568 <213> ORGANISM: artificial
```

```
                RAW SEQUENCE LISTING              DATE: 09/25/2000
                PATENT APPLICATION:  US/09/659,983    TIME: 12:45:58

                Input Set : A:\ES.txt
                Output Set: N:\CRF3\09252000\I659983.raw

      570 <220> FEATURE:
W--> 572 <221> NAME/KEY: Xaa
      574 <222> LOCATION: 1
      576 <223> OTHER INFORMATION: pyroglutamic acid
W--> 578 <221> NAME/KEY: Xaa
      580 <222> LOCATION: 5
      582 <223> OTHER INFORMATION: amino acid substitution
W--> 584 <221> NAME/KEY: Xaa
      586 <222> LOCATION: 6
      588 <223> OTHER INFORMATION: D-Lys
W--> 590 <221> NAME/KEY: Xaa
      592 <222> LOCATION: 11
      594 <223> OTHER INFORMATION: Gly or Gly preceded by spacer
W--> 596 <221> NAME/KEY: Xaa
      598 <222> LOCATION: 15
      600 <223> OTHER INFORMATION: amino acid substitution
W--> 602 <221> NAME/KEY: Xaa
      604 <222> LOCATION: 16
      606 <223> OTHER INFORMATION: D-Lys
W--> 608 <221> NAME/KEY: Xaa
      610 <222> LOCATION: 21
      612 <223> OTHER INFORMATION: Cys-NH2
      614 <400> SEQUENCE: 11
      616     Xaa His Trp Ser Xaa Xaa Leu Arg Pro Gly Xaa His Trp Ser Xaa Xaa
      617     1               5                   10              15
      618     Leu Arg Pro Gly Xaa
      619                     20
      621 <210> SEQ ID NO: 12
      623 <211> LENGTH: 21
E--> 625 <212> TYPE: peptide
      627 <213> ORGANISM: artificial
      629 <220> FEATURE:
W--> 631 <221> NAME/KEY: Xaa
      633 <222> LOCATION: 1
      635 <223> OTHER INFORMATION: pyroglutamic acid
W--> 637 <221> NAME/KEY: Xaa
      639 <222> LOCATION: 6
      641 <223> OTHER INFORMATION: D-Lys
W--> 643 <221> NAME/KEY: Xaa
      645 <222> LOCATION: 7
      647 <223> OTHER INFORMATION: amino acid substitution
W--> 649 <221> NAME/KEY: Xaa
      651 <222> LOCATION: 11
      653 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 655 <221> NAME/KEY: Xaa
      657 <222> LOCATION: 16
      659 <223> OTHER INFORMATION: D-Lys
W--> 661 <221> NAME/KEY: Xaa
      663 <222> LOCATION: 17
```

```
                    RAW SEQUENCE LISTING              DATE: 09/25/2000
                    PATENT APPLICATION:  US/09/659,983    TIME: 12:45:58

                    Input Set : A:\ES.txt
                    Output Set: N:\CRF3\09252000\I659983.raw

        665 <223> OTHER INFORMATION: amino acid substitution
W--> 667 <221> NAME/KEY: Xaa
        669 <222> LOCATION: 21
        671 <223> OTHER INFORMATION: Cys-NH2
        674 <400> SEQUENCE: 12
        676      Xaa His Trp Ser Tyr Xaa Xaa Arg Pro Gly Xaa His Trp Ser Tyr Xaa
        677      1               5                   10              15
        678      Xaa Arg Pro Gly Xaa
        679                   20
        682 <210> SEQ ID NO: 13
        684 <211> LENGTH: 21
E--> 686 <212> TYPE: peptide
        688 <213> ORGANISM: artificial
        690 <220> FEATURE:
W--> 692 <221> NAME/KEY: Xaa
        694 <222> LOCATION: 1
        696 <223> OTHER INFORMATION: pyroglutamic acid
W--> 698 <221> NAME/KEY: Xaa
        700 <222> LOCATION: 6
        702 <223> OTHER INFORMATION: D-Lys
W--> 704 <221> NAME/KEY: Xaa
        706 <222> LOCATION: 9
        708 <223> OTHER INFORMATION: amino acid substitution
W--> 710 <221> NAME/KEY: Xaa
        712 <222> LOCATION: 11
        714 <223> OTHER INFORMATION: Gly or Gly preceded by a spacer
W--> 716 <221> NAME/KEY: Xaa
        718 <222> LOCATION: 16
        720 <223> OTHER INFORMATION: D-Lys
W--> 722 <221> NAME/KEY: Xaa
        724 <222> LOCATION: 19
        726 <223> OTHER INFORMATION: amino acid substitution
W--> 728 <221> NAME/KEY: Xaa
        730 <222> LOCATION: 21
        732 <223> OTHER INFORMATION: Cys-NH2
        735 <400> SEQUENCE: 13
        737      Xaa His Trp Ser Tyr Xaa Leu Arg Xaa Gly Xaa His Trp Ser Tyr Xaa
        738      1               5                   10              15
        739      Leu Arg Xaa Gly Xaa
        740                   20
```

```
                    VERIFICATION SUMMARY              DATE: 09/25/2000
                    PATENT APPLICATION:  US/09/659,983    TIME: 12:45:59

                    Input Set : A:\ES.txt
                    Output Set: N:\CRF3\09252000\I659983.raw

L:17  M:270 C: Current Application Number differs, Replaced Application Number
L:19  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:57  M:310 E: (3) Wrong or Missing Sequence Type, TYPE:              .
L:63  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:69  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:85  M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:91  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:97  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:114 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:120 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:133 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:139 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:145 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:152 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:171 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:177 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:183 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:189 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:201 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:207 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:222 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:228 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:234 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:240 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:246 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:252 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:258 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:264 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:282 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:288 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:294 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:300 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:306 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:312 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:324 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:343 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:349 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:355 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:361 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:367 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:373 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:379 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:397 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:403 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:409 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
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VERIFICATION SUMMARY                    DATE: 09/25/2000
PATENT APPLICATION:   US/09/659,983     TIME: 12:45:59

Input Set : A:\ES.txt
Output Set: N:\CRF3\09252000\I659983.raw

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L:415 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:421 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:433 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:439 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:445 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:451 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:472 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:478 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:484 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:490 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:496 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:502 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:519 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:566 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:625 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:686 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
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